

#3

## CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/509, 472

CRF Edit Date: 10-7-04  
Edited by: KL

Realigned nucleic-acid/amino-acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

**ENTERED**

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

~~\_\_\_\_\_~~

Deleted:  invalid beginning/end-of-file text;  page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/509,472

DATE: 10/07/2004  
TIME: 10:37:57

Input Set : A:\pto.kd.txt  
Output Set: N:\CRF4\10072004\J509472.raw

3 <110> APPLICANT: University of Utah Research Foundation  
 5 <120> TITLE OF INVENTION: ELASTIN PREVENTS OCCLUSION OF BODY VESSELS BY VASCULAR  
 SMOOTH  
 6 MUSCLE CELLS  
 8 <130> FILE REFERENCE: HYDR-PWO-005  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,472  
 C--> 11 <141> CURRENT FILING DATE: 2004-09-27  
 13 <150> PRIOR APPLICATION NUMBER: 60/368084  
 14 <151> PRIOR FILING DATE: 2002-03-27  
 16 <160> NUMBER OF SEQ ID NOS: 6  
 18 <170> SOFTWARE: PatentIn version 3.2  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 2260  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <400> SEQUENCE: 1  
 26 ctcgagaaga gagggcgtcca gctccccaca gtagccccctg cttccctcct tcccaggcag 60  
 28 gcgaggcac gcagatatac cattgacttc ccctccccctg cagcaggcac atcctggca 120  
 30 tcgagcttca gaccctgccc ctgagcagcc cctaaccctt ccaacaaagg gtggcttggg 180  
 32 ggggcttca cccacgcata atctccatca gctaccctca aagcacccccc aaataaacac 240  
 34 acaccgttaag taagagctgt acactggctg tgcgttaca tcttcagac aattctccca 300  
 36 gcatgcccct accttccaaa attccagagc tgctccctcc aaagaccagg ggaaaaggaa 360  
 38 gggtttgcctc agggtcctgg ggtggccccc tatagaccaa agcctgataa ctgtcctaga 420  
 40 agcagagtagt ttgcagagcg agtgcggca actgtgttat tgacaccgt cctagcacca 480  
 42 gctgaacaca gagcattttt gatctagcaaa aaatacaaga ccacgttgc tttgtcttg 540  
 44 caataatctc tttagcttaga atactgatca cctgttagaca gataaggaaa ctgtatgtct 600  
 46 gtggagaggt ttcccttacca gaaaggctag agccagaaat ttacttcttag gtccaccaat 660  
 48 acctgcctt gaccaatgcc tgcatattgac cttccacgc tgagccaccc ctgtggcac 720  
 50 tccagactgc cacagtgtc ctgcctccac aagggtctt taactcatcc ctgcggacca 780  
 52 tcgtggtgca gggaaaagcc cacaggcgt gtggcttcca tgctgttccc tgactggctg 840  
 54 tgaccttagga caaggaacaa gttccctct cctattctt aggtctcaca ttcttctcc 900  
 56 tctagcagta gtggaaagtg aggggtgggg gacacgaccc tccccgttca catcccacac 960  
 58 tccaaaccctt aaaatccccc agggtccccg tccagctcag tccctggggc agaaatgcag 1020  
 60 agttctccag gaacgtggtc ccagctgttt cagtgcggc cggcccttcc tggccaccag 1080  
 62 cggaaatgtca gccttccac agggccggg agaacagcag tggagaagct cccagactgg 1140  
 64 tggggcgct agctgtgtc agcgtggggta tgggaggtga cccagtgata atggaaagct 1200  
 66 gggctgcctg tcagtctgtg gggggctccc acctccctgt tccccccacag ggcacctggg 1260  
 68 gatccagcct gattttacc agacctgcgg cctgcattgg gctgggtata gggctgtgac 1320  
 70 cttgaccctt gcagaataga accctgtgtg tgggatcct ccatgtgtc cagatgcccc 1380  
 72 tggggacago accaacatgg ctttaactcc caagccattc ccctgcctt aacccttgg 1440  
 74 catctgcagg catccacccc agacccaccc aacaccttcc cccagcttc aggccgttgg 1500  
 76 cagagacctt ggcccttgca gaatgcggcc ctgtccagg tccccctactt tccccccaga 1560  
 78 tccctccac agcaatacca acccgccctt accttccagg ccattcaacc tgcagccccc 1620  
 80 cggccctgtt agacatgcga ccccccacac cccagaccc tccctccccc 1680

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82 agctttgggc agaacctgtc tctagccaga cctgggggtg ttggggagtc tggagggccg 1740  
 84 ggggtggggc tgaggcgcgg gacagctggc ccgtatcctc acactggcc cagccggagg 1800  
 86 ggcgggggccc tggccactcg ggccttggct ggggctggga tttttggcct ggccgcccagg 1860  
 88 ccctcccttc tgcttcctct cccgagggtc gtcctggcag aggccccctc cgctcttct 1920  
 90 ggcgggaaaca gggccagcag cggaaagaaca gtcgcagagg gaaagcggga aagagatggg 1980  
 92 ggaaaagtgtg tgtgtgtgag tgtgtgttg tgtgcatgtg tgtgcgtgtg ttgtgtcaag 2040  
 94 aaaaaagctc gcagtccagc agccggggcc tgggaggctt gtgagccggg ccttcgtaa 2100  
 96 ttgtcccttc cccgcggccc cctcccccag gcctccccc tctcccgccc tccggccgc 2160  
 98 cctctctccc tccctcttcc cctcacagcc gacgaggcaaa caatttaggtt ttggggataa 2220  
 100 aacgaggtgc ggagagcggg ctggggcatt tctccccggag 2260  
 103 <210> SEQ ID NO: 2  
 104 <211> LENGTH: 757  
 105 <212> TYPE: PRT  
 106 <213> ORGANISM: Homo sapiens  
 108 <400> SEQUENCE: 2  
 110 Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Pro Gly Val Leu Leu Leu  
 111 1 5 10 15  
 114 Leu Leu Ser Ile Leu His Pro Ser Arg Pro Gly Gly Val Pro Gly Ala  
 115 20 25 30  
 118 Ile Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly Ala Gly Leu  
 119 35 40 45  
 122 Gly Ala Leu Gly Gly Ala Leu Gly Pro Gly Gly Lys Pro Leu Lys  
 123 50 55 60  
 126 Pro Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala Gly Leu Gly  
 127 65 70 75 80  
 130 Ala Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro Gly Gly Val  
 131 85 90 95  
 134 Ala Asp Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu  
 135 100 105 110  
 138 Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val  
 139 115 120 125  
 142 Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val  
 143 130 135 140  
 146 Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala Arg Phe  
 147 145 150 155 160  
 150 Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys  
 151 165 170 175  
 154 Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val  
 155 180 185 190  
 158 Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile  
 159 195 200 205  
 162 Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly  
 163 210 215 220  
 166 Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly  
 167 225 230 235 240  
 170 Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala  
 171 245 250 255  
 174 Ala Ala Ala Ala Lys Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly  
 175 260 265 270

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Input Set : A:\pto.kd.txt  
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178 Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala  
179 275 280 285  
182 Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala  
183 290 295 300  
186 Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala  
187 305 310 315 320  
190 Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val  
191 325 330 335  
194 Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro  
195 340 345 350  
198 Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val  
199 355 360 365  
202 Ser Pro Glu Ala Ala Ala Lys Ala Ala Lys Ala Ala Lys Tyr Gly  
203 370 375 380  
206 Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly  
207 385 390 395 400  
210 Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly  
211 405 410 415  
214 Val Ala Gly Val Pro Ser Val Gly Gly Val Pro Gly Val Gly Gly Val  
215 420 425 430  
218 Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Lys  
219 435 440 445  
222 Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala Ala Ala Ala Lys Ala  
223 450 455 460  
226 Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala  
227 465 470 475 480  
230 Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly  
231 485 490 495  
234 Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly  
235 500 505 510  
238 Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala  
239 515 520 525  
242 Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala  
243 530 535 540  
246 Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro  
247 545 550 555 560  
250 Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly  
251 565 570 575  
254 Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu  
255 580 585 590  
258 Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro  
259 595 600 605  
262 Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys  
263 610 615 620  
266 Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly  
267 625 630 635 640  
270 Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro  
271 645 650 655  
274 Ala Ala Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln Phe

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Input Set : A:\pto.kd.txt  
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275 660 665 670  
 278 Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu  
 279 675 680 685  
 282 Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala  
 283 690 695 700  
 286 Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly  
 287 705 710 715 720  
 290 Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe  
 291 725 730 735  
 294 Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys  
 295 740 745 750  
 298 Gly Arg Lys Arg Lys  
 299 755  
 302 <210> SEQ ID NO: 3  
 303 <211> LENGTH: 6  
 304 <212> TYPE: PRT  
 305 <213> ORGANISM: Artificial Sequence  
 307 <220> FEATURE:  
 308 <223> OTHER INFORMATION: A bioactive fragment of tropoelastin.  
 310 <400> SEQUENCE: 3  
 312 Val Gly Val Ala Pro Gly  
 313 1 5  
 316 <210> SEQ ID NO: 4  
 317 <211> LENGTH: 6  
 318 <212> TYPE: PRT  
 319 <213> ORGANISM: Artificial Sequence  
 321 <220> FEATURE:  
 322 <223> OTHER INFORMATION: Control random fragment.  
 324 <400> SEQUENCE: 4  
 326 Val Ser Leu Ser Pro Gly  
 327 1 5  
 331 <210> SEQ ID NO: 5  
 332 <211> LENGTH: 582  
 333 <212> TYPE: DNA  
 334 <213> ORGANISM: Homo sapiens  
 336 <400> SEQUENCE: 5  
 337 atggctgcca tccgaaagaa actggtgatt gttggtgatg gagcctgtgg aaagacatgc 60  
 339 ttgctcatag tcttcagcaa ggaccagtgc ccagagggtt atgtgccac agtggtag 120  
 341 aactatgtgg cagatatcga ggtggatgga aagcaggtag agttggctt gtggacaca 180  
 343 gctgggcagg aagattatga tcgcctgagg cccctctcct acccagatac cgatgtata 240  
 345 ctgatgtgtt tttccatcga cagccctgtat agtttagaaa acatcccaga aaagtggacc 300  
 347 ccagaagtca agcatttctg tcccaacgtg cccatcatcc tggttggaa taagaaggat 360  
 349 ctcggatag atgagcacac aaggcgggag ctagccaaga tgaagcagga gcccgtgaaa 420  
 351 cctgaagaag gcagagatata gcaaacaagg attggcgctt ttgggtacat ggagtgttca 480  
 353 gcaaagacca aagatggagt gagagaggtt tttgaaatgg ctacgagagc tgctctgcaa 540  
 355 gctagacgtg ggaagaaaaa atctggttgc cttgtcttgtt ga 582  
 358 <210> SEQ ID NO: 6  
 359 <211> LENGTH: 193  
 360 <212> TYPE: PRT

RAW SEQUENCE LISTING  
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Input Set : A:\pto.kd.txt  
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361 <213> ORGANISM: Homo sapiens  
363 <400> SEQUENCE: 6  
365 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys  
366 1 5 10 15  
369 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu  
370 20 25 30  
373 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu Val  
374 35 40 45  
377 Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu  
378 50 55 60  
381 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile  
382 65 70 75 80  
385 Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro  
386 85 90 95  
389 Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile  
390 100 105 110  
393 Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu His Thr Arg  
394 115 120 125  
397 Arg Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Glu Glu Gly  
398 130 135 140  
401 Arg Asp Met Ala Asn Arg Ile Gly Ala Phe Gly Tyr Met Glu Cys Ser  
402 145 150 155 160  
405 Ala Lys Thr Lys Asp Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg  
406 165 170 175  
409 Ala Ala Leu Gln Ala Arg Arg Gly Lys Lys Lys Ser Gly Cys Leu Val  
410 180 185 190  
413 Leu

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/509,472

DATE: 10/07/2004

TIME: 10:37:58

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\10072004\J509472.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date